

## FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG  
CTCTGTTGAGAATCATGCCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC  
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC  
AGACTGCAGTAAGTGTTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGC  
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT  
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG  
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT  
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT  
GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG  
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC  
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT  
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG  
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCTTGCTCTTTG  
AACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT  
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT  
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTACAGGGGCTCAGAA  
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATACTCAGCATCTTTATCAC  
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT  
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG  
AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA  
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG  
TGTTACAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTC  
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG  
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCACTTCGGATGTGGGGTCAGGAGGTTG  
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA  
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACTATTAATAAATACCTT  
AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT  
ATGGAATAAACACACCTTTGTTAAAGATAAAAAAAA

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## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP  
GIPGNHGNNGNNGATGHEGAKGEKGDKDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL  
ATHFSNQNSGIIIFSSVETNIGNFFDVMGTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG  
NTVFSMYSYEMKGKSDTSSNHA VLK LAKGDEVWLRMGNGALHGDHQRSTFAGFLLFETK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Motif name: Clq domain signature.**

amino acids 137-167

**Clq domain proteins.**

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

protein database

### FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG  
CTCTGGCAGGCTCCTGGCAGCATGGCAAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT  
GGGCCTGGCCCAGCCAGCCTCTGCCC GCCGGAAGCTGCTGGTGTCTTCTGCTGGATGGTTTTT  
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGC  
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA  
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACC  
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGG  
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA  
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTGAGACCCACCTACTGCCTAGAATATAAAA  
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT  
GGCCGGGCCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG  
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA  
CCAAGTGGATCCAGGAGCGGGGCCTGCAGGACCGCCTGAACGTATTATTTCTCGGATCAC  
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA  
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC  
ACTCTGAGATATATAACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC  
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA  
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA  
GGCGGGAAGGTTGGCAGCGTGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC  
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACTTCAGAGCTGCTCCTATCAGGTGGT  
GGACGTCTACAATGTGATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT  
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGC  
CACTGTGCCCTGGCACTGATTCTTCTCTTCTGCTTGCATAACTGATCATATTGCTTGTCTC  
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA  
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT  
TCTATACATAAAAGTTCCTACTTGTTAA

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## **FIGURE 4**

MAVKLGTLALLLALGLAQPASARRKLLVFLLDGFRSDYISDEALESIPGFKEIVSRGVKVDY  
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVKNKDSLMPPLWWNGSEPLW  
VTLTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA  
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRNLNVIIFSDHGMTDIFW  
MDKVIELNKYISLNDLQQVKDRGPVVSLLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFY  
KKGKFFVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP  
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI  
LLFLLA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

#### **N-myristoylation sites.**

amino acids 148-154, 365-371

#### **Amidation site.**

amino acids 343-347

## FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCC  
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG  
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCA  
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG  
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG  
TGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCACCAGCGCTCCATCTCACC  
CTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT  
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG  
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT  
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGGCTGCACCT  
GCGTGCTGCCCCGTTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGC  
TCCCCAGAGGGCACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCCAACACT  
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC  
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA  
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA  
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT  
TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

[illegible]

Important features:

amino acids 1-18

## amino acids 112-121

amino acids 32-38, 55-61, 133-139

amino acids 3-25

## amino acids 99-195

[illegible][illegible]

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP

LVTKMCHIGCPDIPSLGLGPYVSIACCQTS LCNHD

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 6-11 and 33-38

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 24-34 and 78-88

10036244-10036244



## FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAG  
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCT  
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG  
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG  
CTGGGCTCGGGCGGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTAGAGTC  
GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG  
CCGCG**ATG**AGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC  
TTCTGCCGCCGCGTGGTCAAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA  
CAAAATGGCCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT  
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG  
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTCTGATGGTGATTTCTGGATAGG  
GCTTTGGAGGAATGGAGATGGGCAAACATCTGGTGCTGCCAGATCTCTACCAGTGGTCTG  
ATGGAAGCAATTCCCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG  
TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA  
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA  
ATCCAACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT  
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC  
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTA  
AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA  
GAAAGTGGCATGGAAGTAT**TA**ATAACTCATTGACTTGGTTCAGAATTTTGTAAATCTGGATC  
TGTATAAGGAATGGCATCAGAACAATAGCTTGGAATGGCTTGAAATCACAAAGGATCTGCAA  
GATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTATATGTCTATTATTTT  
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC  
CCAACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC  
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTA  
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAGTATTTTACCTTTGCATAA  
GTGTTTGATAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT  
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG  
TACCATAGAAAAAGTTTGTTTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA  
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTTATTAAGTGTGATATAAACCTCCTC  
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA  
TTATTTTTTAGCTTAAAATTAAACAGATTTTGTAAATAATGTAACCTTTGTTAATAGGTGCATAA  
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA  
CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTCTGAAATCAATGTGGTCCCTCTC  
TTGCCCACTAAACAAAGATGGTTGTTGCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC  
AAAGTTAGTCTAAGGTTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG  
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC  
ATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAAATGGGTGGAAACCATCAGTGATCG  
CATATTCATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC  
TAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCTGGTCTTCA  
TATGTCCCTGTGCTCCTTTTAACCAATAAAGAGTTCTTGTCTTGGGGGAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACE  
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDWFGLWRNGDGQTSGACPDLYQWSDG  
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNHYICKYEPEINP  
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG  
RTKTSPNQSTLWISKSTRKESGMEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 214-235

#### **N-glycosylation sites.**

amino acids 86-89 and 255-258

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

#### **N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

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GAGGAAATGAGAGAGACAGTGGAGAGTGGAGTCCGGGGTCTGGTCGGGGTGGTCTGTCTGCTCTGGCATGCCCTG  
 CCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCTGGGTCTGTGTGCGAGGCCGGCAGGTGG  
 GCGTGAAGGGCACAGACCGCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC  
 GGTCTCAGCCCCACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCAGCTCGGCCCCCAATGTGCCTAC  
 AAGAGCTGGAGAGCATGAACAGCAGCAGATTTTGTCTCAACGGAAAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
 GCGTGGTCTCAACGTCTATAGCCACAGTGAAGTCCCCGAGGGTCCGGTAGGCCGCTCATGGTATGGGTCCATG  
 GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTGG  
 TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
 TCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
 CTGTCTTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTCTGCTCCCACTGGCTGCGAGGCTGTCTCC  
 ACAGAGCCATCACACAGATGGGTGCATCACCAACCCAGGGATCATCGACTCTCACCTTGGCCCTAGCTCAGA  
 AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
 AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
 GCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
 GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
 CAACACCCGCTCTTGACCAGTCTGGATGTGCCCTCTGAGATGATGCCACCGCTCATAGATGAATACCTAGGAAGCA  
 ACTCGGAGCACAAGCCAAATGCCAGGCGTCCAGGAATTCATGGTGACGTATTCATCAATGTTCCCAACCGTCA  
 CTTTTTCAAGATACTTTCGAGATCTGGAAGCCCTGTCTTTTTCTATGAGTTCCAGCATCTGACCCAGGACTTTTGT  
 CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTGTGTTGCGAGGTCCCTTCTCA  
 TGGACGAGAGCTCCCGCTGGCCTTTCAGAGGGCCACAGAGGAGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
 AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTTGCCCTCCTTGGCCCCAATTCAACCAGGCGG  
 AACAAATATCTGGAGATCAACCCAGTGCCACCGGCCGAGCAGAAGTTCAGGAGGCTGGATGGCAGTTCTGGTCAG  
 AGACGCTCCCCAGCAAGATACAAGTGGCAGCAGAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTCTGAGGCC  
 AGGCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCAGCACGGCAGCCCGCTCTC  
 CCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGA  
 ATGTCACAAGGCCGCTCCACCTCTGGGCATTGTACAAGTCTTCCCTCTCCCTGAAGTGCCTTTCCTGCTTT  
 CTTCGTGGTAGGTTCTAGCACATTCCTCTAGCTTCTCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC  
 TGGGCTGTGCGGCCCGAGTCTCGCTCCATTAGACAGACAGTCCACCCGAGGCTAGCCGTGTGTGTCTGTCT  
 CCCCCTCAGAGGAGCTCTCTCAAATTGGGATTAGCCTAACCCCACTGTGTCAACACACAGGATCGGGTGGGA  
 CCTGGAGCTAGGGGGTGTCTTGTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC  
 CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCCACCAGCATTGTCCACCCTGGCCAGAAGGGTGCATGCC  
 AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCCTGAC  
 TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCTCTCTCTGCTGCCAGCTCTGGCCCCCTGCACAAGACAACAGA  
 ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTACCAATTCCAGCCCCCTGACCCTCAGGACGCTGGATG  
 CCAGCTCCACAGCCCCAGTGCCGGGTCTCTCTCTCTCTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG  
 AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGCGGCTATTGTACA  
 GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACAAGAGGTTTTAGATGGAAGTGAGAG  
 GTGACAGTGTGCTGCCAGCCCTCACAGCCCTCGCTTGTCTCTCTCGCCCTGCGCCTCTGCCTGGGCTCCCACTTTGGCA  
 GCATTTGAGAGGCCCTTCAACCCCGCTGCATCTGAGTAGGAGCCCCCTTCTGGGCTGGCCAAGCCGAGCCAGCT  
 CCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGGGGCCAG  
 AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT  
 TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCTTAGCTGCCTCCCGCGGGGAGGGCTCGG  
 GACCTGCAGCCCTCCATGCCTGACCTCCCCCACCACCCCGTGGGCTCCTGTGCGGCGGAGCCTCCCCAAGGAG  
 CGCGGCCCTCTGCTCCACAGCGCCCACTCCCATCGACCAACCAAGGGCTGAGGAGTGCGGGTGACAGCGCGGGA  
 CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGCTGGATCCATGGGTGAAGCAGCTGGGCTCTGAGTCTGGTGG  
 GGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAATACACCGATGGGCACCTCTGTATCTAGCTCAAGGTT  
 TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTTTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
 ACTCTGGTGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGAGAACT  
 TTGTGCTAGCTCAGGGATCGTAACCGACCAATCAGCACCTGTGTCAAAACAGACCACTTGACTCTGTGTAAT  
 GGACCAATCAGCAGGATGTGGTGGGCGAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCATGACAACCC  
 CCTCGGGTCCCCTCCACGCGCTGGAAGCTTTGTTCTTTCTGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGVKGTDRLVNVFLG  
IPFAQPPLGPD RFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC  
LVLNVYSPA EVPAGSGRPVMVWVHGGALITGAATSYDGSALAA YGDVVVTVQYRLGVLGFF  
STGDEHAPGNQGF LDVVAALRWVQENIAPFGGDLNCVTVF GGSAGGSIISGLVLS PVAAGLF  
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT  
IYPLTVDGT VFPKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLD TMEQMSREDMLA  
ISTPVLTS LDVPPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS  
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM  
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW  
HQQQKNRKAQEDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-27

#### **Transmembrane domain:**

amino acids 226-245

#### **N-glycosylation site.**

amino acids 105-109

#### **N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

#### **Carboxylesterases type-B serine active site.**

amino acids 216-232

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## FIGURE 13

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAG  
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAATAAAATTCCTCAA  
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCT  
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG  
ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCCTTCAGCGTG  
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATC  
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT  
CTGAAGGAGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAAT  
TTTTGGAAGTATCTTGTCAACCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC  
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG  
AGGATCTATGAAGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG  
GTCTCATTTTAAACATTTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG  
CAGTAGTGCGTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCA  
ATGAAGGATTTTTTTTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAG  
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACT  
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG  
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT  
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG  
GAATAAAACACAAATGTTGAAAAATGTAAATATATATACATAGATTCAAATCCTTATATAT  
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTCTTTTAAAGTACAGGTTCCTAGTGTTTT  
ACTATAACTGTCACTATGTATGTAAGTACATATATAAATAGTCATTTATAAATGACCGTAT  
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAA

1036214-12604

## **FIGURE 14**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSL  
EKYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFCNQFGESEPRPSKEVES  
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEP  
IEVIRPDIAALVRQVVIKKKEDL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Glutathione peroxidases signature 2.**

amino acids 104-112

**Glutathione peroxidases.**

amino acids 57-82

10036214-132601

## FIGURE 15

TGTCGCCCTGGCCCTCGCCATGCAGACCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA  
CTGGGGGGGCGCCACGGCCTCTTTCTGAGGAGCGCGCGCCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTGTTGTGGGCAGCGGGCCCCGACGCGCTGACCCCCGAGAGGCTGCTGACGACCTCAACATCCAGCGA  
GTCTGCGGGTCAACAGGACGCTGTTCAATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGGATGAAG  
GGCAAAACAGGAGGGCGAGTGTGCGAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTTCCAACGCCTTCAACCCGGTGTGCGCAACTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC  
GGTATGGCCCGCTGCCCCGTACGACCCCAAGCACGCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT  
ACTGTTACCGACTTCTAGCCATTGATGCTGTCTATCTACCGCAGCGCTCGGGGACAGGCCACCCCTGCGCACCGTG  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
TTCCGGGAGATTGCGATGGAGTTTAACCTACCTGGAGAAGGTGGTGGTGTCCGCGTGGCCCGAGTGTGCAAGAAC  
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGCTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA  
CCCCGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTACGCTCGGGGGCGGGCCCGTG  
GTCCTGGCCGTTTTTTCCACGCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG  
GCAGCTGTGTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGCTGCCGGAGGATCAG  
GTGCCCTGACCCCGGGCCCGGTGCTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCTTGGCCGATGAC  
ATCCTCAACTTTGTCAAGACCCACCCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCTGGATCCTG  
CGGACCTGATGAGGCACACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGCAACACAGACCGTT  
GTCTTCTGGGTTCTGAGGCGGGGACGGTCTCAAGTCTCTCGTCCGGCCCAATGCCAGACCTCAGGGACGTCT  
GGGTCAGTGTCTTCTGGAGGAGTTTGAGACCTACCGGCCGACAGGTGTGGACGCGCCGGCGGTGGCGAGACA  
GGGACGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTCCCCGCTGCGTGGT  
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTACGACCCCTACTGC  
GGGTGGGCCCCCGACGGCTCCTGCATCTTCTCAGCCCCGGGCACACAGAGCCGCTTTGAGCAGGACGTGTCCGGG  
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG  
TCGGTGAACCTGCTGGTAACGTGCTCGGTGGCGGCCCTCGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC  
TGTTTCGTGGGCCTCCGTGAGCGCGGGAGCTGGCCCGCGCAAGGACAAGGAGGCCATCTGGCGCACGGGGCG  
GGCGAGGCGGTGCTGAGCGTCAGCGCCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGCGGAGGCGGT  
GGCGTGGCGCGGGGTTCCCCGGAGGCCCTGCTGGCGCCCTTGAGACCCAGCCTCAGCCGCGGATGGCTCCCGCG  
CTGCAGGGCGGGCCCCACGACCTGGAATCGGGGCTGCTGCCACGCCCGAGCAGACGCCGTGCCGCAAGCGC  
CTGCCACTCCGACCCCGCACCCCCACGCCCTGGGCCCGCGCCTGGGACCACGGCCACCCCTGCTCCCGGCC  
TCCGCTTCATCCTCCTCCTGCTGCTGGCGCCCGCGGGCCCCCGAGCAGCCCCCGCGCTGGGGAGCCGACC  
CCCGACGGCCGCTCTATGCTGCCCGGGCCCGCGCGCCTCCACGGCGACTTCCCGCTACCCCCCACGCCAGC  
CCGGACCGCGCGGGTGGTGTCCCGGCCACGGGCCCTTGAGACCCAGCCTCAGCCGCGGATGGCTCCCGCG  
CCCTGGAGCCCGCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCTGCGC  
CGCACCCACAGTTCAACAGCGGCGAGGCCCGGCCCTGGGACCGCCACCGCGGCTGCCACGCCCGCGGGGACA  
GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGCCCTAGGCCGGGGGCCCCCG  
ATGCCCTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGCGGTGCCAGAACGCCGGGGCCCGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCGCGACCCACCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAACCAG  
CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTECTATG  
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTGCAGTTTTGGTTTTCTTTGCGTTTTCTAAC  
AATTGCACAACCTCCGTTCTCGGGGTGGCGGCAGGACGGGAGGCTTGGACGCCGTGGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG  
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCCGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG  
TGGGCGTGTGTGCAAGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCAGAAGGCCGGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC  
CCCCCCTCTGCAAGAGGAAGCGGGACAATGCCGGGTTTCAGGCAGGAGACACGAGGAGGGCTGCCCGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGCGAAGGTGGGTGGGGCCCTCTGTAA  
ATACGGCCCCAGGGTGGTGAGAGAGTCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCTCCCCAGCCCCCTCCCCATCAAT  
AAAACCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 16**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAGHLFPEEPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGA  
DDLNIQRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG  
ECRNFVKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF  
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFREI  
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSPVPGDSHFYFNVLQAVTG  
VVSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPVEDQVPR  
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHPWILRTLMRHQLTRVAVDV  
GAGPWGNQTVVFLGSEAGTVLKLFLVRPNASTSGTSGLSVFLFEEFETYRPDRCGRPGGGETGQ  
RLLSLELDAASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPG  
TRAAFEQDVSGASTSGLGDCGTGLLRASLSEDRAGLVSVNLLVTSSVAAFEVVGAVVSGFSVGW  
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGRGGGGGGGAGVPPEALLA  
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLP  
SASSSLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRVVSAPTG  
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG  
TDLAHLPPYGGADRTAPPVP

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domains:**

amino acids 318-339, 598-617

#### **N-glycosylation sites.**

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466

#### **Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

#### **N-myristoylation sites.**

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885



## FIGURE 17

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCCTCGGCCGGGACAGC  
AGAACGCCAGGGGACCCCTCACCTGGGCGCGCCGGGGGCACGGGCTTTGATTGTCCTGGGGTCG  
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG  
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC  
ATTTATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT  
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCCG  
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT  
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT  
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCCTAGAGTTGGAGTCCAGGTTTTAGAC  
CGAAAAGATGGGTCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAATCTGAAGGT  
GGAAATTAAATTCGAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAAGGGCCGGTTT  
ACCATGAGAACTGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC  
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA  
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA  
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT  
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT  
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCTGGT  
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG  
GAAACCATGGGCCGGGTAAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCTTCCCTG  
GGAAAGCAAAAATTCCACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC  
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC  
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTTCATTTTTTGATTTCTT  
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC  
TAGTTGGTGACAGTGTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAG  
CTGCAGCCCTGGAAACACTACATTCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT  
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG  
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT  
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC  
TGAGGACGACCTCTTCCCTTGTAATGTCATAGGAAAAAGACCAAAGATGAACTCTGATATG  
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT  
TTTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA  
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTAGAAATTTTATAA  
TAAAACCACCTTTATTTTAAAGGAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVLPARYFYIQAVDTSGNKF  
TSSPGEKVFQVKVSAPEEQFTRVGVQVLDKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKS  
PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR  
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNS  
NIHPIFSWCGSTDSDKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR  
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV  
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWKAKDHDEEAKK  
IAKAGQEFARNNLMGDDIFCYFVKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK  
KTKDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-glycosylation sites.**

amino acids 302-306, 414-418

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

#### **Tyrosine kinase phosphorylation site.**

amino acids 341-348

#### **N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

#### **Endoplasmic reticulum targeting sequence.**

amino acids 499-504

## FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA  
GCCTAGCGTGTCCACGATGCGGGCTGGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATCG  
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCC  
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCTCGGCTGGAGCCAGTTCTAACTG  
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG  
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAA  
AAAGGAGCATCTCACAGTTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT  
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTCGACGTCATCAGGAACCTCAATTCTC  
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT  
TATGGAGATGAAACCTGGGTAAATTATTCCCAAAGCATTTTGTGGAATATGATGGAACAAC  
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG  
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC  
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT  
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAAATTTGCTGG  
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG  
GTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA  
TCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA  
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAG  
CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC  
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGGGAAC  
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAAGTCTTCAACCTGGGCTCCAAGGTT  
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA  
GTTCTCACCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT  
CCCCTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTCGGCCG  
TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG  
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGG  
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGG  
TGTCCCGACACAGGTGTTACATCTGTGCTGTGAGGTGAGATGCCTCAGTTCTTGAAAGCT  
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCC  
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGA  
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTTCGACCAC  
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGA  
CGTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTTCGTTAGCTGGGGAGTG  
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG  
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATC  
CCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT  
TGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGC  
CCATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA  
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

10036214.12601

## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPP  
PLFSKVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT  
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVS  
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHT  
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208

TOGETHER

[illegible][illegible]

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL  
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA  
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSPVYIIRTCHR  
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 233-251

#### **N-glycosylation sites.**

amino acids 120-124, 174-178

#### **N-myristoylation sites.**

amino acids 15-21, 84-90

## FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG  
GAAAGGACAAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT  
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGCTGT  
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT  
CCTTGGCAGGTTCTGGGTTTGGACGTTATTTCGGTGAAGTGAAGGAAACAGAGAAAGGATCCTTT  
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCG  
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCA  
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT  
CAAATTTTAATGGATGATCCCTTTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA  
TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG  
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA  
AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT  
GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT  
TAACCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC  
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGGCCAGGCTCTGTATGAGACCCAGGC  
TCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG  
GAGTCAACGCGGAAGTATCCTATTCATTTTTTGTATGCCTCAGAAAATATTCGAACGACCTTT  
CAAATCAATCCTTTTTCTGGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA  
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCTTTCTGCAAGATGTAGGGTTT  
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAAGTATCGTATCATCATTTTCCAAC  
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC  
TGGAGAAAATGGAAAGATGGTTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT  
CTGTGGAGAATTTTTACATCTTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG  
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAAT  
AACGGTCTTGGTCTCCGACGTCAATGACAACGCCCCCGCCTTCACCCAAACCTCCTACACCC  
TGTTCTGTCGCGGAGAACACAGCCCCGCGCTGCACATCGGCAGCGTCAGCGCCACAGACAGA  
GACTCGGGCACCAACGCCAGGTCACCTACTCGCTGCTGCCGCCCCAAGACCCGCACCTGCC  
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTGCTGG  
ACTACGAGGCCCTGCAGGCTTTTCGAGTTCGCGCTGGGCGCCACAGACCGCGGCTCCCCCGCG  
CTGAGCAGAGAGGCGCTGGTGCAGCTGCTGGTGTGGACGCCAACGACAACCTCGCCCTTCGT  
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGGAGC  
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG  
TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTTCGGTGTGTGGGCGCACAAATGGGGA  
GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCGAGCCAAGCACAGGCTCGTGGTGTG  
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGTCTCCTGGTGGAC  
GGCTTCTCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGGCCAGGCCAGGCCGAGGC  
CGACTTGCTCAGCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTCTCT  
CGGTGCTCCTGTTCTGTCGGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG  
TGCTCGGTGCCCCAGGGTCCTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT  
GTCCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAGTGAGTTCAAGT  
TCTTGAAACCAGTTATTTTCGGATATTTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT  
TCCACCTTCCGAAATAGCTTTGGATTTAATATTCAGTAAAGTCTGTTTTTAGTTTTCATATAC  
TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTTAAATCTCAAATTTAAGTTAT  
TATGCAACTTCAAGCATTTATTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTCATCAT  
TTTTTTGCATTAAATAACAACAGGTTTAAATTTAATGAGTATTTTTTTCTAAATGATAGTGT  
AAGGTTTTAATTCTTTCCAACAGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT  
CTGAGGTTTTGATTCAATTTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTG  
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATT  
CGTGTGTTGAAAACCATGTCAATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC  
TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAATAC  
CCTTAGTTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTGCCAATATTTT  
CTTATGTTAACTTTTGTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA  
ATCTGCCTGAAAATGAATAAAATAAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

## FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR  
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR  
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHINISGGD  
EGMIYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVLVDVNDNAPQFAQALYE  
TQAPENSPIGFLIVKVAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE  
LVNSYKINIQAAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND  
RDSGENGKMVCYIQENLPFLKPSVENFYILITEGALDREIRAENITITVTDLGTPRLKTE  
HNITVLVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSTNAQVTYSLLPPQDP  
HLPLASLV SINADNGHLFALRSLDYEAQAFEFVVGATDRGSPALSREALVRVLVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQAO  
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGA  
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

### Important features of the protein:

#### Signal peptide:

amino acids 1-26

#### Transmembrane domain:

amino acids 687-711

#### N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

#### Glycosaminoglycan attachment site.

amino acids 28-32

#### Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

#### N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

#### Amidation site.

amino acids 781-785

#### Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

#### Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560



## FIGURE 25

GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTC  
GTCTTCCTTCCGGGGGACAACGTGGGTCAGGGCACAGAGAGATATTTAATGTCACCCTCTTG  
GGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTC  
AGAACTCCAGCCTA**ATG**GATCCCAAACCTCGGGAGAATGGCTGCGTCCCTGCTGGCTGTGCTG  
CTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCTCCCCGCCCCGGCGCTGTTAGAGAA  
AGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGG  
CCATCGAGAGCAGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTCTTCAGAATGATG  
GCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTCC  
TCAGCAGCTGCCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACCTGGGGA  
GCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCGG  
GGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTTATGGACG  
AGGAGCGACCGACAACAAAGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAG  
CCCTGGAGCAAGATCTTCCTGTGAATATCAAATTCATCATTTGAGGGGATGGAAGAGGCTGGC  
TCTGTTGCCCTGGAGGAACTTGTGGAAAAAGAAAAGGACCGATTCTTCTCTGGTGTGGACTA  
CATTGTAATTTTCAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAACCC  
GGGGGAACAGCTACTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCACTCAGGAACC  
TTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGA  
CTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGG  
AAATAAATACATACAAAGCCATCCATCTAGACCTAGAAGAATACCGGAATAGCAGCCGGGTT  
GAGAAATTTCTGTTTCGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCT  
TTCTATTTCATGGGATCGAGGGCGCGTTTGATGAGCCTGGAACATAACAGTCATACCTGGCC  
GAGTTATAGGAAAATTTTCAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAA  
CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAACAAGATGGTTGT  
TTCCATGACTCTAGGACTACACCCGTGGATTGCAAATATTGATGACACCCAGTATCTCGCAG  
CAAAAAGAGCGATCAGAACAGTGTTTGGAAACAGAACCCAGATATGATCCGGGATGGATCCACC  
ATTCCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGCTGGG  
AGCTGTTGATGATGGAGAACATTCGCAGAATGAGAAAATCAACAGGTGGAACCTACATAGAGG  
GAACCAAATTATTTGCTGCCTTTTTCTTAGAGATGGCCCAGCTCCAT**TAA**TCACAAGAACCT  
TCTAGTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAAT  
GTAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAATGTCTTG  
GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAGGTCC  
CCCACTGCACACCTTCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCCAAGTCCTGT  
GCAATAGCCCCAGGATTGGATTCCTTCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGA  
TTGGCATAATCACTCCGGTTTGCTTTCTAGGTCCTCAAGTGCTCGTGACACATAATCATTCC  
ATCCAATGATCGCCTTTGCTTTACCACTCTTTCCTTTTATCTTATTAATAAAAAATGTTGGTC  
TCCACCACTGNCTCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAA

10035214.12601

## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD  
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEFGSDPTK  
GTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD  
LPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIIVISDNLWISQRKPAITYGTRGNSY  
FMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY  
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK  
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI  
RTVFGTEPDMIRDGSTIPIAKMFQEIIVHKSIVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF  
A AFFLEMAQLH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

273-292

#### **N-glycosylation sites.**

amino acids 322-326, 382-386, 402-406

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 400-404

#### **N-myristoylation sites.**

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,  
351-357

#### **Cell attachment sequence.**

amino acids 140-143

#### **ArgE / dapE / ACY1 / CPG:**

amino acids 156-167

## FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCTGGGAATTTAAGGGACCCACACTACCTTCC  
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGT**CATG**GGACCTGTGCGGTT  
GGGAATATTGCTTTTCTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG  
AGGACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG  
CTACAGGCGGAAGTGAAGTGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT  
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG  
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA  
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG  
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT  
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC  
TTCCACCATCAGGAGCAGCCCCACAAAATTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC  
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA  
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG  
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAG  
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG  
CTTTCAGGGTGTGTTTATGAGTGAAGTCCACCCAAAGCTTGTAGCTGTTCTCTCCCATCTAACC  
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG  
TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA  
CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCAACCAAAAGTCAGCAGTGGCACTGGAGC  
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCTTCCAAGGAAGA  
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA  
GCAAACCGTGAAGGAGAATGGGACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGG  
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT  
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

## **FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL  
ELGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK  
GLVQKGVKVDLGIPLLEWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG  
HVLPAETAQLQETWTGKEITDGEKTEGEEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

#### **N-myristoylation site.**

amino acids 115-121

#### **Amidation site.**

amino acids 70-74

1003624-42604

## **FIGURE 29**

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT  
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG  
T TACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA  
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTCTACCCAGAGTTGG  
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACACTACAGACAGAAGATCACCTCCTGG  
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT  
GGATCCAGATGCCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA  
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATT CAGGGCCAGGAGTTATCAGCCTAC  
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA  
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAAAATGG  
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG  
AACTACCAGGACTCACCAACCCTCCAGGCTCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA  
AACCAGGCAGAGAT**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC  
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA  
ATTAAAAAAAAAATCATCAA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP  
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK  
KGKIQQQELSA YQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL  
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 169-173

#### **Tyrosine kinase phosphorylation site.**

amino acids 59-68

#### **N-myristoylation sites.**

amino acids 54-60, 83-89, 130-136

#### **Phosphatidylethanolamine signature.**

amino acids 113-157

## FIGURE 31

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTTCAGTCCCCTGGACTGTAGATAAAGA  
CCCTTTCTTGCCAGGTGCTGAGACAACCACACTATGAGAGGCACTCCAGGAGACGCTGATGG  
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG  
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG  
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT  
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT  
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC  
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA  
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT  
TTTCGTCTACATTTTCTTAGTGTCATTTTACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG  
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG  
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCCTCTCAAGCTGGTGCTGTGTAG  
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA  
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA  
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT  
ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAGACCTTGTAACA  
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC  
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA  
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAG  
ACCTTGTAACAATAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCTTAATTGTAATGTG  
TAATCTTAAAGTTAAATAAAGTTTGTGTATTATATAATAATAAAGCTAAAGCTGATATAAA  
ATAAAGAAAGAGTAAACTG

## **FIGURE 32**

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL  
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY  
NTAFELNIND

### **Signal sequence:**

amino acids 1-17

### **N-myristoylation site.**

amino acids 10-16

### **Cell attachment sequence.**

amino acids 36-39

10035914 122604



Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 ± 2.0
Marital status	
Married	40 (80.0%)
Single	10 (20.0%)
Occupation	
Retired	30 (60.0%)
Unemployed	20 (40.0%)
Income (USD/month)	1000.0 ± 500.0
Health status	
Good	30 (60.0%)
Poor	20 (40.0%)
Comorbidities	
Hypertension	15 (30.0%)
Diabetes	10 (20.0%)
Cholesterol	12 (24.0%)
Smoking status	
Smoker	10 (20.0%)
Non-smoker	40 (80.0%)
Alcohol consumption	
Regular	5 (10.0%)
Occasional	15 (30.0%)
Never	30 (60.0%)
Family size	3.0 ± 1.0
Living alone	10 (20.0%)
Living with family	40 (80.0%)
Health insurance	
Yes	35 (70.0%)
No	15 (30.0%)
Medication use	
Regular	20 (40.0%)
Occasional	10 (20.0%)
Never	20 (40.0%)
Healthcare utilization	
Regular	15 (30.0%)
Occasional	10 (20.0%)
Never	25 (50.0%)

GCGAGGCTGCACCAGCGCCTGGCACCATGAGGACGCCTGGGCCTCTGCCCCGTGCTGCTGCTG  
CTCCTGGCGGGAGCCCCGCGCGGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC  
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT  
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG  
CGGGACTTTGTGGCCTCGCCCCCGTGTGGAAAGTGGCCCAGGTAGATTCTTTGAAGGACAA  
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCTGTGTG  
ATGACTGCAATGCCTTGAATACCCAATCCCACTGACTACGGTCCTGCCAGATCGTCAGCGC  
TAAGGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT  
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAACTGTTATGTA  
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCTTACCAGGAACCTCCTTTGAGCATAGA  
GTTAGCAACCATGCTTCTCATTCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC  
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAACTA  
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA  
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTTCTAACAC  
AGACTTTCTTCACTGTCTTTTCAATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG  
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC  
ACATGGA

## **FIGURE 34**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY  
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLLDDCNALEYF  
IPVTTVLPDRQR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Tyrosine kinase phosphorylation site.**

amino acids 60-69

#### **N-myristoylation site.**

amino acids 16-22

## FIGURE 35

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA  
CTTGACTCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA  
GCCGCCAGTCCCGGCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTAC  
TCCTCCTTTTTCATTACATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA  
AGCCGAGCGTGGAAGAATGAGGGGTTCTTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCC  
CGATTCAAGCTTTCCTCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA  
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAATAAAAC  
ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGC  
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA  
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA  
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC  
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT  
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTAT  
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT  
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG  
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG  
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA  
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG  
AAAAGTATTGATTTCAGAAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC  
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT  
CCTACCTTGAAAACCTTGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAT  
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA  
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA  
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT  
TTGGAAGCCATCAGAAAAAATATTTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA  
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA  
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAATAA  
TGGAAGGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAACACTTC  
TAATTCTGTGATTAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT  
TAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCCGTAAAACTATCTGAAAGTAAAGT  
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 36**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN  
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK  
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA  
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDET  
VSNTLTLTNGLERRTKTYSEDNFEELQYFPN FYALLKSIDSEKEAKEKETLITIMKTLIDFV  
KMMVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE  
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS  
KMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 37

GTTGCTCCGGCGGGCGCTCGGGGAGGGAGCCAGCAGCCTAGGGCCTAGGCCCGGGCCACC**ATG**  
GCGCTGCCTCCAGGCCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTCTGAG  
CTCAGGTTGGGGGGAGTTGGAGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGCACTTC  
GGGAGAATGAACGCCACGCCTTCACCTGCCGGGTGGCAGGGGGGGCCTGGCACCCCCAGATTG  
GCCTGGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCGTGGGAGG  
GGAGGCCCTTCTCTGGAGGCACCAGCACCTTCACTGTCACTGCCCATCGGGCCCCAGCATGAGC  
TCAACTGCTCTCTGCAGGACCCAGAAAGTGGCCGATCAGCCAACGCCTCTGTCACTCCTTAAT  
GTGCAATTCAAGCCAGAGATTGCCCAAGTCGGCGCCAAGTACCAGGAAGCTCAGGGCCCCAGG  
CCTCCTGGTTGTCTGTGTTGCCCTGGTGCCTGCCAACCCGCCGGCCAATGTACCTGGATCG  
ACCAGGATGGGCCAGTGACTGTCAACACCTCTGACTTCTGGTGCTGGATGCGCAGAACTAC  
CCCTGGCTCACCAACCACACGGTGCAGCTGCAGCTCCGCAGCCTGGCACACAACCTCTCGGT  
GGTGGCCACCAATGACGTGGGTGTCAACAGTGCCTCGCTTCCAGCCCCAGGGCCCCCTCCCGGC  
ACCCATCTCTGATATCAAGTGACTCCAACAACCTAAACTCAACAACGTGCGCCTGCCACGG  
GAGAACATGTCCCTCCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATTCAGAGCAGT  
GAAACCAGCAGACCGGCAGATGGCTCAGAACAACAGCCGGCCAGAGCTTCTGGACCCGGAGC  
CCGGCGGCCTCCTCACAGCCAAGGTTTCATCCGCCTCCAGTGCTGGGCTATATCTATCGA  
GTGTCCAGCGTGAGCAGTGATGAGATCTGGCTC**TGA**GCCGAGGGCGAGACAGGAGTATTCTC  
TTGGCCTCTGGACACCCCTCCCATTCCTCCAAGGCATCCTCTACCTAGCTAGGTACCAACGT  
GAAGAAGTTATGCCACTGCCACTTTTGCTTGCCCTCCTGGCTGGGGTGCCCTCCATGTCTG  
CACGTGATGCATTTCACTGGGCTGTAACCCGCAGGGGCACAGGTATCTTTGGCAAGGCTACC  
AGTTGGACGTAAGCCCCCTCATGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGGCCCTT  
CCAGAGGGAGCTCTTTGGCCAGGGGTGTTGAGATGTGATCCAGCATCCAAGTGTTGGCATGGC  
CTGCTGTATACCCACCCCACTCTCCACAGCACCTTGACAGTAGGCATGGGGGCGTGCCT  
GTGTGGGGGACAGGGAGGGGCCCTGCATGGATTTTCCTCCTTCCCTATGCTATGTAGCCTTGT  
CCCTCAGGTAAAATTTAGGACCCTGCTAGCTGTGCAGAACCAATTGCCCTTTGCACAGAAA  
CCAACCCCTGACCCAGCGGTACCGGCCAAGCACAAACGTCCTTTTGTGCTGCACACGTCTCTG  
CCCTTCACTTCTTCTCTTCTGTCCCCACCTCCTCTTGGAATTCTAGGTTACACGTTGGACC  
TTCTCTACTACTTCACTGGGCACTAGACTTTTCTATTGGCCTGTGCCATCGCCAGTATTAG  
CACAAAGTTAGGGAGGAAGAGGCAGGCGATGAGTCTAGTAGCACCCAGGACGGCTTGAGCTA  
TGCATCATTTTCTACGGCGTTAGCACTTTAAGCACATCCCCTAGGGGAGGGGTGAGTGAG  
GGGCCCAGAGCCCTCTTTGTGGCTTCCCCACGTTTGGCCTTCTGGGATTCACTGTGAGTGTC  
CTGAGCTCTCGGGGTTGATGGTTTTTCTCTCAGCATGTCTCCTCCACCACGGGACCCAGCC  
CTGACCAACCCATGGTTGCCTCATCAGCAGGAAGGTGCCCTTCCCTGGAGGATGGTCGCCACA  
GGCACATAATTCAACAGTGTGGAAGCTTTAGGGGAACATGGAGAAAGAAGGAGACCACATAC  
CCCAAAGTGACCTAAGAACACTTTAAAAAGCAACATGTAAATGATTGGAAATTAATATAGTA  
CAGAAATATATTTTCCCTTGTTGAGATCTTCTTTTGTAAATGTTTTTTCATGTTACTGCCTAGG  
GCGGTGCTGAGCACACAGCAAGTTTAATAAACTTGAATGAATTCATTTAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 38**

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR  
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL  
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN  
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLP  
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY  
RVSSVSSDEIWL

### **N-glycosylation sites:**

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

### **Glycosaminoglycan attachment site:**

amino acids 23-27

### **Casein kinase II phosphorylation sites:**

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

### **N-myristoylation sites:**

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

[illegible]

CGGGGACGGAAGCGGGCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGCGATGTTGGAGCGC  
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG  
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC  
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA  
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGC  
GCTCGGAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG  
CATGTGCTTACGGGCAAGAACCTGCACACGCACCATTCCCGTCGCCGCTGTCCAACAACCA  
GGAGGTGAGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT  
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG  
TTCTGTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG  
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA  
GTGTGGAGCCCTCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGG  
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC  
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

Variable	Mean	SD	Min	Max
Age	34.5	10.2	18	65
Gender	0.45	0.50	0	1
Marital status	0.60	0.49	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.70	0.46	0	1
Smoking status	0.30	0.46	0	1
Alcohol consumption	0.20	0.40	0	1
Exercise frequency	0.10	0.30	0	1
Stress level	0.50	0.50	0	1
Sleep quality	0.60	0.49	0	1
Work satisfaction	0.40	0.50	0	1
Life satisfaction	0.50	0.50	0	1
Depression score	10.0	10.0	0	40
Anxiety score	15.0	15.0	0	60
Quality of life score	70.0	10.0	50	100

><subunit 1 of 1, 221 aa, 1 stop

MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS  
GSGQQSVTGVEASDDANSYWRIIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPL  
SNNQEVSAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH  
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Signal peptide:

Glycosaminoglycan attachment site.

N-myristoylation sites.

Endoplasmic reticulum targeting sequence.

amino acids 218-223



## FIGURE 41

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACACAG  
ACGTGAGCCACTCCACCCAGCCTAAAACTTCATCTTCTTTGGATGAGATGAACACTTTTAAC  
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT  
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAACTTACACA  
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT  
CGTCATCATGTCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA  
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG  
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT  
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTTGGCCAAAAGTACTGCA  
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC  
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT  
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA  
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG  
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC  
ACGAGCCAAGTACCTCAAGAGACATGGCTTCTAACATCTCAGATGAAACCCAAGACCATGAT  
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAAGTGGGAAT  
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAACCAAAAAAAAAAAAAA

## **FIGURE 42**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

.><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM  
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTWISE  
SQVSQTTEVLTTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA  
KYLKRHGF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **N-myristoylation sites.**

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

#### **Amidation site.**

amino acids 40-44

## FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAAG  
CCCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC  
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG  
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT  
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG  
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC  
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGAG**  
ACTCATTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT  
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG  
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT  
CCCTTCCCCTTCCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT  
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG  
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA  
AAGGAGGCTCCCATATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA  
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA

[illegible]

><subunit 1 of 1, 125 aa, 1 stop

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN

LRCGTPEEPCQEAFNQTNRKLGLTYNTTCCKNDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Signal peptide:

amino acids 1-18

amino acids 77-81, 88-92

amino acids 84-90

## amino acids 85-98

## FIGURE 45

ACGGGCGCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA  
GTCGGGCGGTTCTTCGCGCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT  
ACCGCACCCAGGTTTCGGCCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCCAT  
GGCGCGAGCCTGCGGGCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTC  
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA  
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA  
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTC  
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA  
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT  
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC  
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCC  
TCGGCGGATTCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT  
TGTAAGTCTATAAGCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC  
CTCCATTTTCCACCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTT  
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGC  
TTTTACAGGACAACAAGGATATGAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAAGTG  
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG  
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA  
TGGAGGCTCGGGCAGCTATTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG  
GATATGGTGGTACCAGGAGACGATAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT  
TTTGGATTTTTCATCACTTTCTCTTTAGAAAAAAGTACTACCTGTTAACAATTGGGAAAAG  
GGGATATTCAAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAG  
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA  
TATTGCAGTTTTTGAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAC  
CTGTGATGCCCTAAGAAGCATTAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA  
AATTTAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA  
TTTGGTATTATATTATTTGATGTTTGTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA  
TTATGCTAATTTGTGAGTTCTGATCACTTTTGTGCTCTGAAGCTTTGAATCATTAGTGGTG  
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA  
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTCTG  
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC  
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

## **FIGURE 46**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP  
QLKCVGGTAGCDSYTPKVIQCQNKGWGDYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY  
VLRGSCGLEYNLDYTELGQLKLGESGKQHGFAFSDYYYKWSSADSCNMSGELITIVVLLGIA  
FVVYKFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS  
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPL  
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 171-190

### **N-glycosylation site.**

amino acids 172-176

### **Glycosaminoglycan attachment sites.**

amino acids 244-248, 259-263, 331-335

### **Tyrosine kinase phosphorylation site.**

amino acids 98-106

### **N-myristoylation sites.**

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318